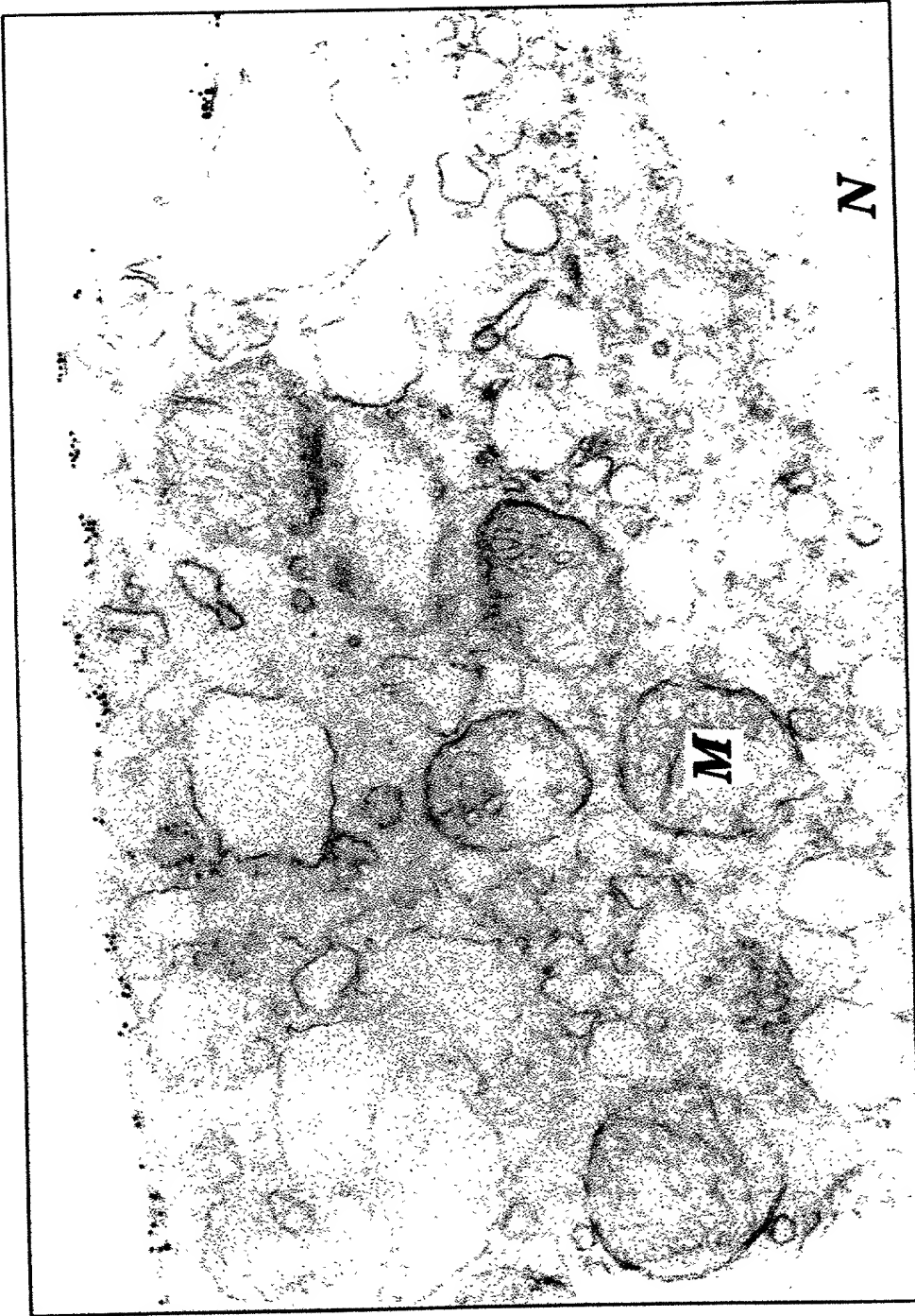


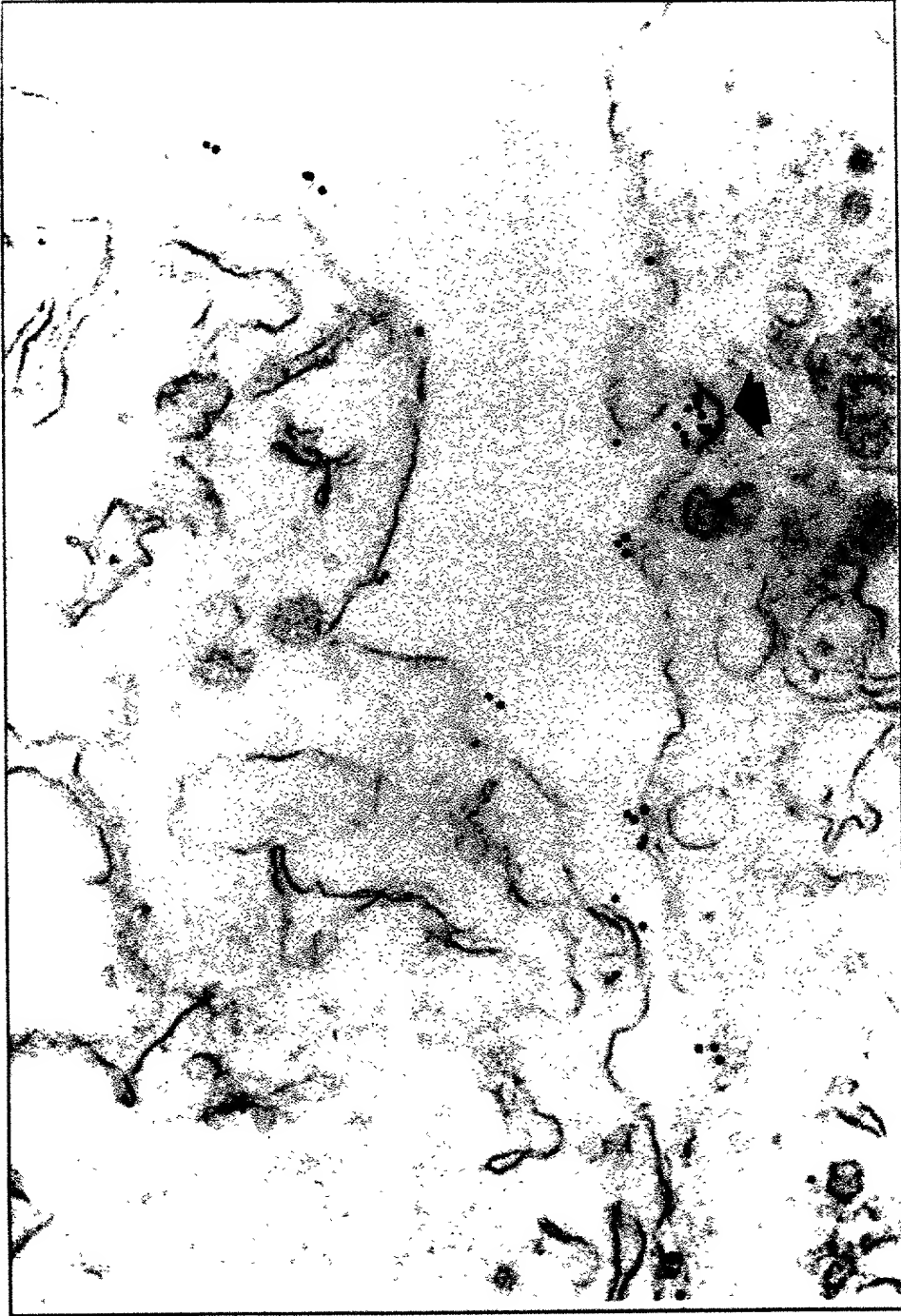
01/11



**FIG. 1**

099665 1001  
T.D.02T" 59962660

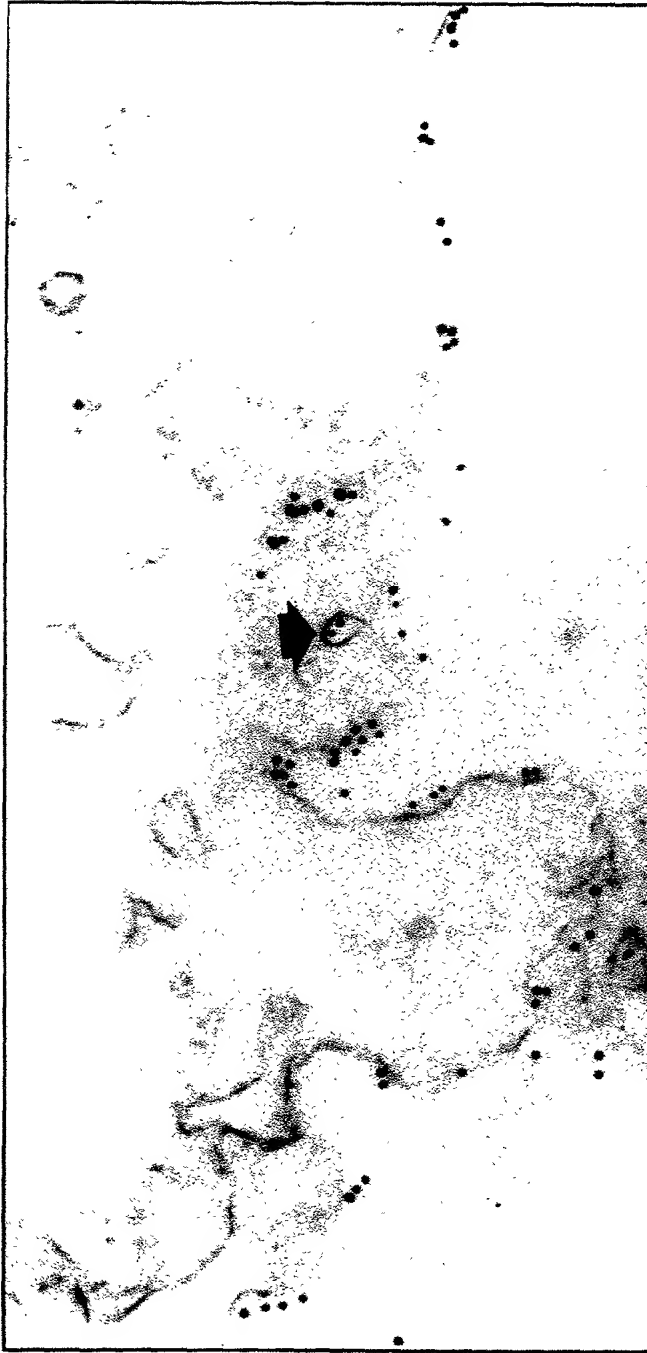
02/11



**FIG. 2**

09929665 120701

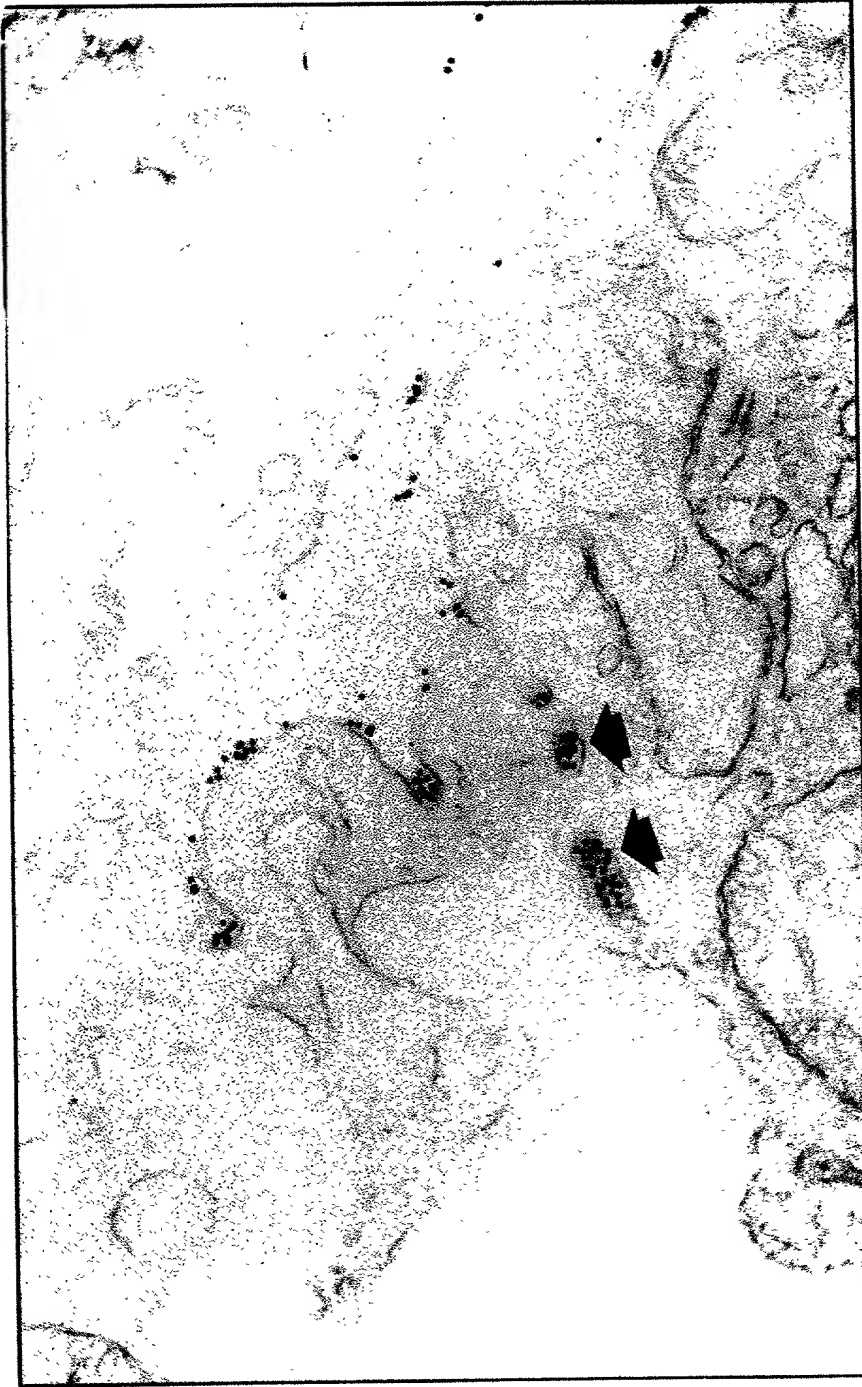
03/11



**FIG. 3**

FOOT " 59962660

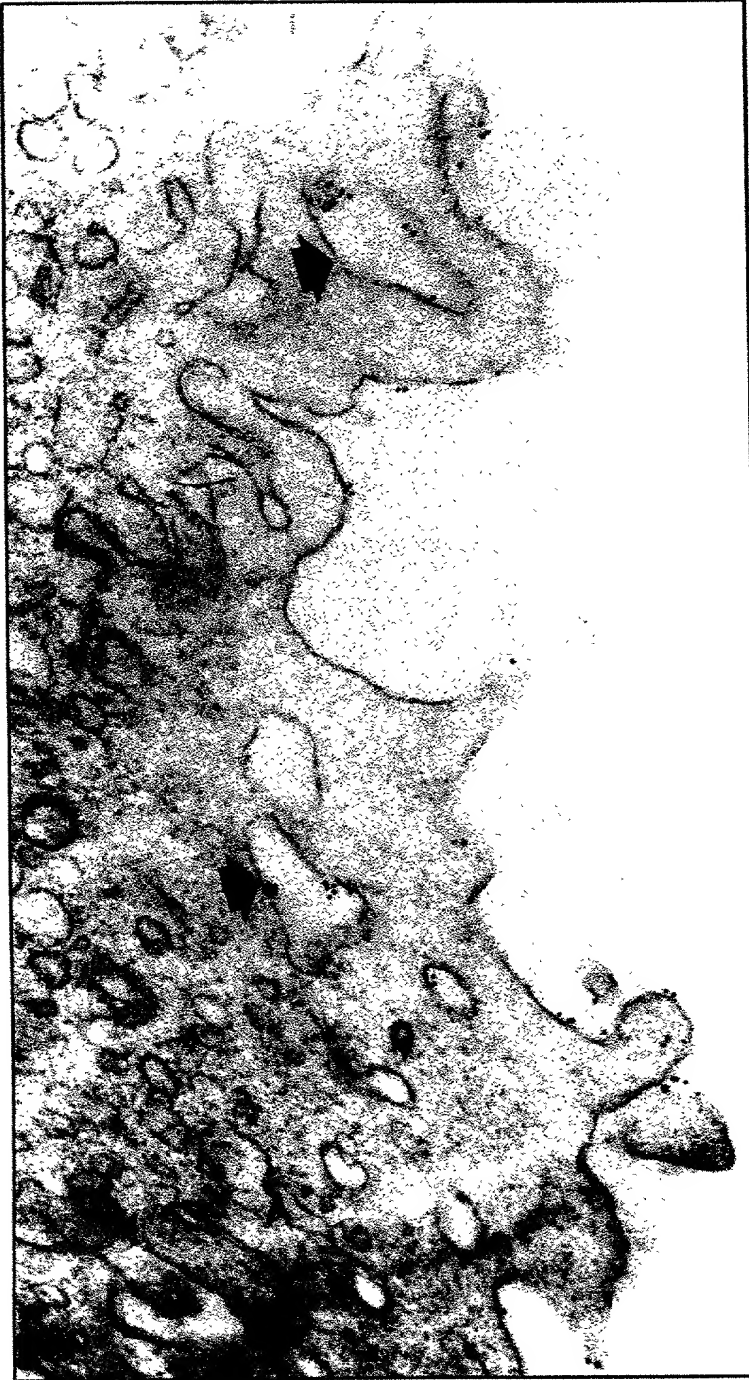
04/11



**FIG. 4**

0999665-10001

05/11



**FIG. 5**

09929665-10701  
TOTAL 59962660

06/11

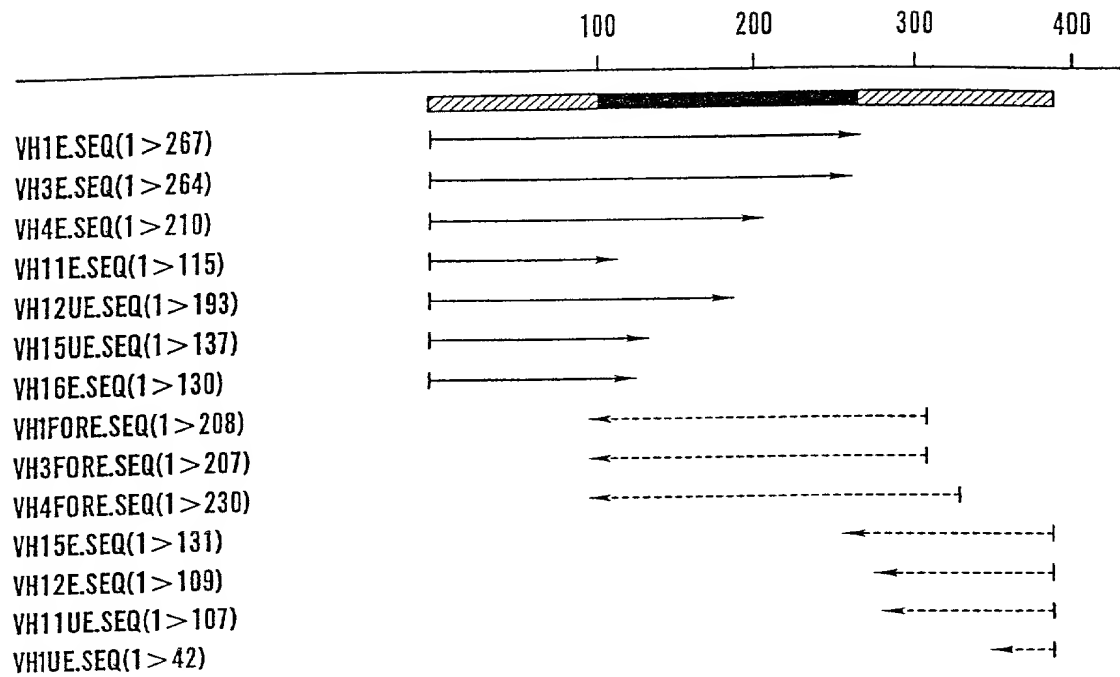


FIG. 6

## TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929,665

07/11

ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

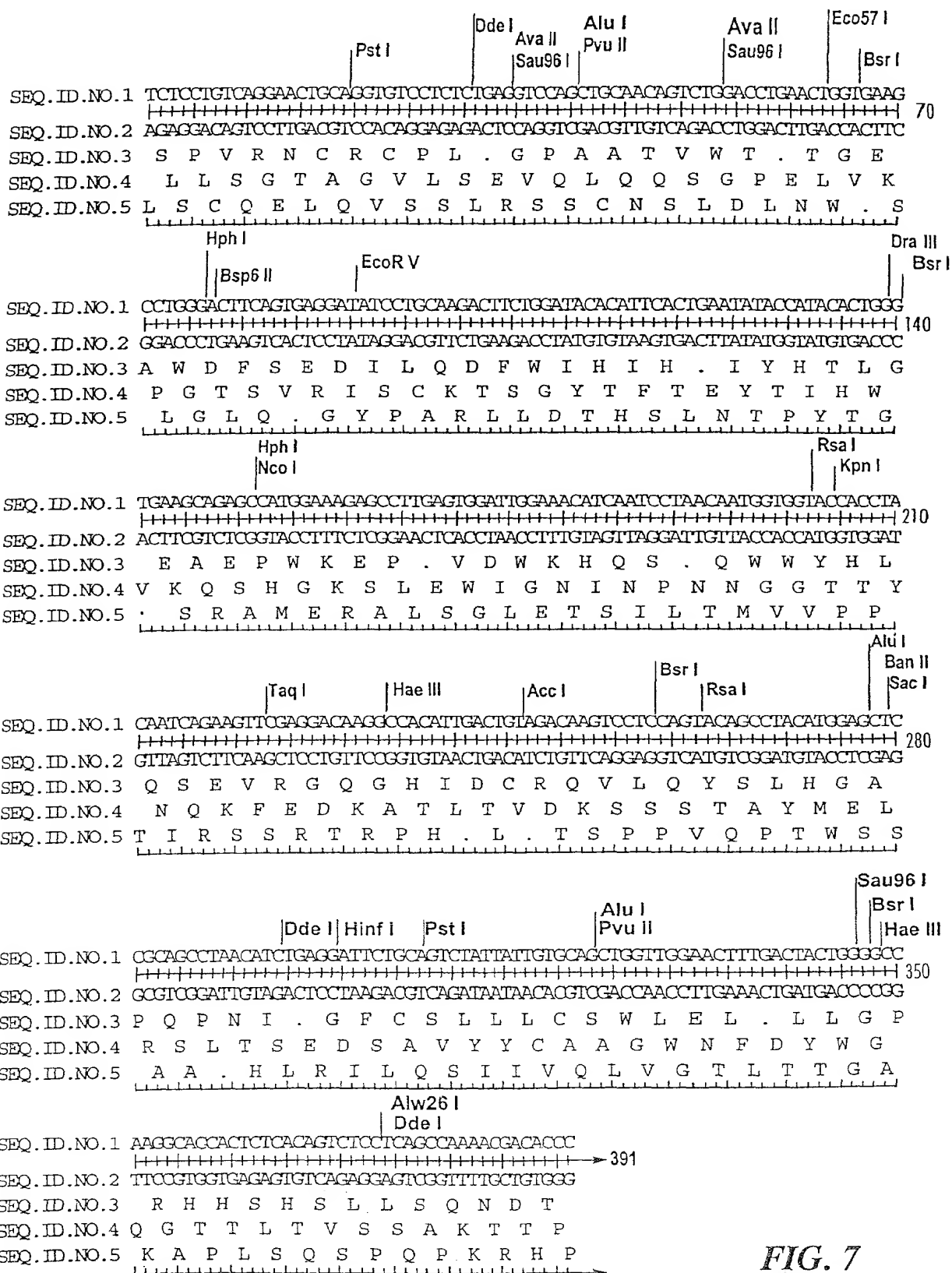


FIG. 7

08/11

## LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGTISVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT  
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:  
EVQLQQSGPELVKPGASVKISCKASGYTFIDYMNWVKQSPGKSLEWIGDINPGNGGIS  
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGIT  
YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGGIT  
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT

LTVSS  
:TVSS  
VTVSS

FIG. 8



TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929,665

09/11

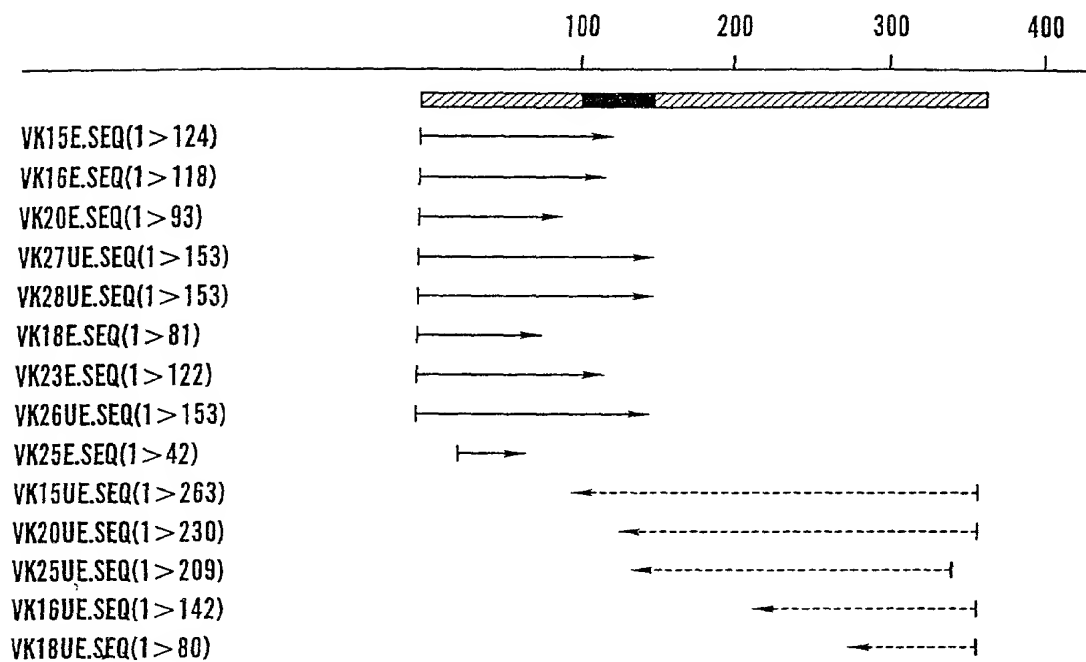


FIG. 9

## TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929,665

10/11

ENZYMES: ALL 74 ENZYMES (NO FILTER):  
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

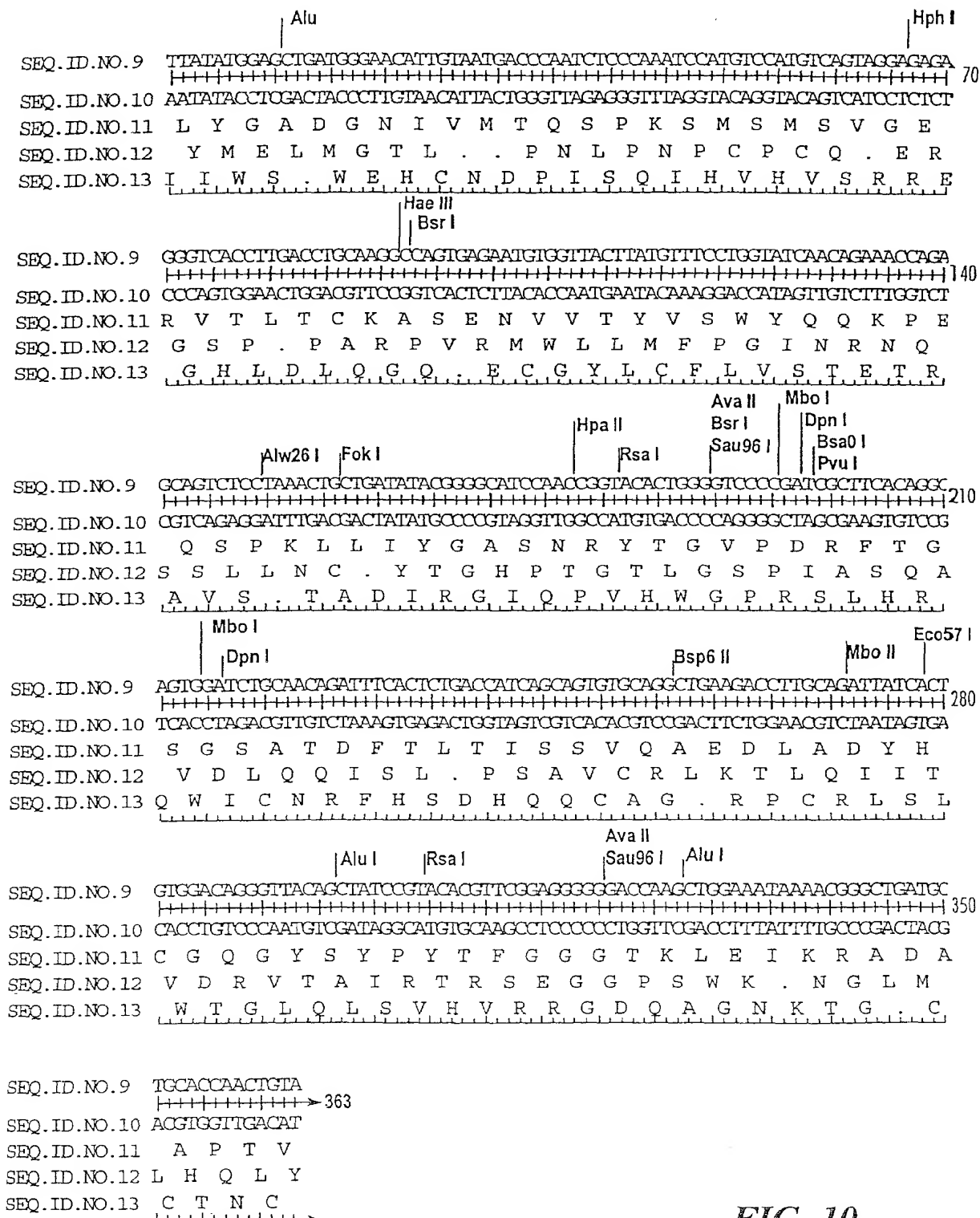


FIG. 10

11/11

## LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1>111)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10      ↓20      ↓30      ↓40      ↓50  
NIVMTQSPKSMMSVGERVILTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP  
:I MIQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQKP. SPKLLIY AS. .:GVP  
DIQMTQSPSSLSASLGDRVITTCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP  
↑10      ↑20      ↑30      ↑40      ↑50      ↑60  
↓60      ↓70      ↓80      ↓90      ↓100  
DRFTGSGSATDFTLTISVQAEDLADYHCGQGY-SY-PYTFGGGKLEIK  
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK  
SRFSGSGSGTDYSLTISNLEQEDIATYFQQGNLPPRTFGGGKLEIK  
↑70      ↑80      ↑90      ↑100

FIG. 11